SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: CIBA-GEIGY AG
 - (B) STREET: Klybeckstr. 141
 - (C) CITY: Basel
 - (E) COUNTRY: Switzerland
 - (F) POSTAL CODE (ZIP): 4002
 - (G) TELEPHONE: +41 61 69 11 11
 - (H) TELEFAX: + 41 61 696 79 76
 - (I) TELEX: 962 991
- (ii) TITLE OF INVENTION: New process for the production of biologically active protein
- (iii) NUMBER OF SEQUENCES: 12
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

	(ii)	MOI	ECUI	E TY	PE:	cDN/	4 to	mRN/	A							
	(iii)	HYE	OTHE	ETICA	AL: N	Ю										
	(vii)				SOURCE:		L LCI	L37/ _E	oPI M t	ı.hT@	GF-be	etal	(DSN	1 565	56)	
	(ix)	FE2	ATURE	E:												
		(2	A) NA	AME/E	ŒY:	CDS										
		(I	3) L(CAT	ON:	33	36									
		(I) O	THER	INFO	RMA!	CION	/pro	oduct	:= "ì	numar	TGE	-bet	:a1"		
											•					
	(xi)	SEÇ	QUENC	CE DE	ESCR	PTIC	ON: S	SEQ :	ED NO): 1:	:					
										ACG						48
ALA 1	Leu	Asp	Thr	Asn 5	Tyr	Cys	Phe	Ser		Thr	Glu	Lys	Asn	-	Cys	
1				3					10					15		
GTG	CGG	CAG	CTG	TAC	ATT	GAC	TTC	CGC	AAG	GAC	CTC	GGC	TGG	AAG	TGG	96
										Asp						30
			20					25	-	-		-	30	•	•	
ATC	CAC	GAG	CCC	AAG	GGC	TAC	CAT	GCC	AAC	TTC	TGC	CTC	GGG	ccc	TGC	144
Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly	Pro	Cys	
		35					40					45				
CCC	TAC	ATT	TGG	AGC	CTG	GAC	ACG	CAG	TAC	AGC	AAG	GTC	CTG	GCC	CTG	192
Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	Leu	Ala	Leu	
	50					55					60					
										GCG						240
	Asn	GIn	His	Asn		Gly	Ala	Ser	Ala	Ala	Pro	Cys	Cys	Val		
65					70					75					80	
CAC	ccc	CTC	GNC	ccc	CTC	ccc	nmc.	Cmc	mac	ma.c	CMC	000	000		200	
CMG	GCG	CIG	GAG	ccu	CIG	uu	ATC	GTG	TAC	TAC	GTG	GGC	CGC	AAG	CCC	288

339

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Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	\mathbf{Tyr}	Tyr	Val	Gly	Arg	Lys	Pro
				85					90					95	
AAG	GTG	GAG	CAG	CTG	TCC	AAC	ATG	ATC	GTG	CGC	TCC	TGC	AAG	TGC	AGC
Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	Lys	Cys	Ser
			100					105					110		
TGA															
(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	10: 2	2:							
		(i) :													
		(2	A) LI	ENGT	1: 1:	l.2 ar	nino	acio	ds						
			3) T												
		(I)T (C	OPOL	GY:	line	ear								
		MO:				-									
	(xi	SE(QUENC	CE DI	ESCR	PTI	ON: S	SEQ :	ID N): 2	;				
		_		_	_										
	Leu	Asp	Thr		Tyr	Cys	Phe	Ser		Thr	Glu	Lys	Asn	_	Cys
1				5					10					15	
Mo 3	7	C1.	T	m	T1.				_	_	_				
val	Arg	Gln		Tyr	тте	Asp	Phe		Lys	Asp	Leu	Gly	_	Lys	Trp
			20					25					30		
T1-	ni e	C1.	D		01										
тте	nls	Glu	Pro	ьуѕ	GTA	Tyr		Ala	Asn	Phe	Cys		Gly	Pro	Cys
		35					40					45			
D	m	~ 1	_	_	_	_									
Pro		Ile	Trp	Ser	Leu		Thr	Gln	Tyr	Ser		Val	Leu	Ala	Leu
	50					55					60				
_															
	Asn	Gln	His	Asn		Gly	Ala	Ser	Ala	Ala	Pro	Cys	Суз	Val	Pro
65					70					75					80
Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	Arg	Lys	Pro
				85					90					95	

Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser 100 105 110

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: E. coli LC137/pPIMu.hTGF-beta2 (DSM5657)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...336
 - (D) OTHER INFORMATION:/product= "human TGF-beta2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
- GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT AAT TGC TGC 48
 Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys
 115 120 125
- CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG GAT CTA GGG TGG AAA TGG 96
 Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp
 130 135 140
- ATA CAC GAA CCC AAA GGG TAC AAT GCC AAC TTC TGT GGT GGA GCA TGC 144

 Lie His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys

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145					150					155					160	
								CAG								192
Pro	Tyr	Leu	Trp	Ser 165	Ser	Asp	Thr	Gln	His 170	Ser	Arg	Val	Leu	Ser 175	Leu	
TAT	AAT	ACC	ATA	AAT	CCA	gaa	GCA	TCT	GCT	TCT	CCT	TGC	TGC	GTG	TCC	240
Tyr	Asn	Thr	Ile 180	Asn	Pro	Glu	Ala	Ser 185	Ala	Ser	Pro	Cys	Cys 190	Val	Ser	
CAA	GAT	TTA	GAA	CCT	CTA	ACC	ATT	CTC	TAC	TAC	ATT	GGC	AAA	ACA	ccc	288
Gln	Asp	Leu 195	Glu	Pro	Leu	Thr	Ile 200	Leu	Tyr	Tyr	Ile	Gly 205	Lys	Thr	Pro	
AAG	ATT	GAA	CAG	CTT	TCT	AAT	ATG	ATT	GTA	AAG	TCT	TGC	AAA	TGC	AGC	336
Lys	Ile 210	Glu	Gln	Leu	Ser	Asn 215	Met	Ile	Val	Lys	Ser 220	Cys	Lys	Cys	Ser	
TAA																339
(2)	INF	ORMA!	PION	FOR	SEQ	ID 1	W: 4	4:								
								rics								
						12 ar no ao		acio	is							
						line										
		MOI														
	(XI)	SEÇ	QUENC	CE DE	ESCRI	IPTIC	ON: S	SEQ :	ED NO): 4:	:					
Ala 1	Leu	Asp	Ala	Ala 5	Tyr	Cys	Phe	Arg	Asn 10	Val	Gln	Asp	Asn	Cys 15	Cys	
Leu	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Lys	Arg	Asp	Leu	Gly	Trp	Lys	Trp	
			20					25					30			

Ile	His	Glu	Pro	Lys	Gly	Tyr	Asn	Ala	Asn	Phe	Cys	Ala	Gly	Ala	Cys
		35					40					45			
Pro		Leu	Trp	Ser	Ser		Thr	Gln	His	Ser	-	Val	Leu	Ser	Leu
	50					55					60				
Tur	Asn	Thr	Ile	Aen	Pro	Glu	a l a	Sar	A1-	202	Dro	Crrc	Crro	17n 1	C
65		****	110	11511	70	OIU	пца	Ser	та	75	FIU	Cys	Cys	Val	80
										,,					00
Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Ile	Gly	Lys	Thr	Pro
				85					90					95	
Lys	Ile	Glu	Gln	Leu	Ser	Asn	Met		Val	Lys	Ser	Cys	Lys	Суз	Ser
			100					105					110		
(2)	INFO	ORMA	TION	FOR	SEO	TD I	vio •	5.							
\- <i>'</i>				. 0	0.00										
	(i) SE	QUEN	CE C	HARA	CTER:	ISTI	CS:							
		(.	A) LI	ENGT	H: 3	39 b	ase j	pair	5						
		(B) T	YPE:	nuc	leic	aci	d							
		(+	C) S	TRAN	DEDNI	ESS:	doul	ole							
		(1	D) To	OPOL	OGY:	lin	ear								
	,														
	(11) MO	LECU:	LE T	YPE:	CDN	A to	mRN.	A						
	(vii) IM	MEDIZ	ATE :	SOUR	Œ:									
			B) C				i LC	137/	pPLM	u.hT	GF-b	eta3	(DSI	M 56	58)
															-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

(D) OTHER INFORMATION:/product= "human TGF-beta3"

(ix) FEATURE:

(A) NAME/KEY: CDS(B) LOCATION:1..336

GCT	TTG	GAC	ACC	AAT	TAC	TGC	TTC	CGC	AAC	TTG	GAG	GAG	AAC	TGC	TGT	48
							Phe									
		115					120					125			•	
GTG	CGC	ccc	CTC	TAC	ATT	GAC	TTC	CGA	CAG	GAT	CTG	GGC	TGG	AAG	TGG	96
							Phe									
	130					135				-	140	-	-	4		
GTC	CAT	GAA	CCT	AAG	GGC	TAC	TAT	GCC	AAC	TTC	TGC	TCA	GGC	CCT	TGC	144
Val	His	Glu	Pro	Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cvs	
145					150					155			_		160	
CCA	TAC	CTC	CGC	AGT	GCA	GAC	ACA	ACC	CAC	AGC	ÁCG	GTG	CTG	GGA	CTG	192
Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu	
				165					170					175		
TAC	AAC	ACT	CTG	AAC	CCT	GAA	GCA	TCT	GCC	TCG	CCT	TGC	TGC	GTG	ccc	240
Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro	
			180					185					190			
CAG	GAC	CTG	GAG	ccc	CTG	ACC	ATC	CTG	TAC	TAT	GTT	GGG	AGG	ACC	ccc	288
							Ile									
		195					200					205				
AAA	GTG	GAG	CAG	CTC	TCC	AAC	ATG	GTG	GTG	AAG	TCT	TGT	AAA	TGT	AGC	336
							Met									
	210					215					220	-	-	-		
rga																320

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp 20 25 30

Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys 35 40 45

Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu 50 55 60

Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro 65 70 75 80

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro 85 90 95

Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "recombinant hybrid DNA of

TGF-beta1 and TGF-beta3 DNA"

(vii)	TMMEDTATE	SOURCE .

(B) CLONE: E. coli LC137/pPIMu.TGF-betal(44/45)beta3

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1.. 132
- (D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-betal"

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 133..336
- (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..336
- (D) OTHER INFORMATION:/product= "hybrid TGF-beta named TGF-beta1-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys

1 5 10 15

GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG GAC CTC GGC TGG AAG TGG 96

Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp

20 25 30

ATC CAC GAG CCC AAG GGC TAC CAT GCC AAC TTC TGC TCA GGC CCT TGC

11e His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Ser Gly Pro Cys

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35

		35					40					45				
CCA	TAC	CTC	CGC	AGT	GCA	GAC	ACA	ACC	CAC	AGC	ACG	GTG	CTG	GGA	CTG	192
Pro	Tyr	Leu	Arg	Ser	Ala	_	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu	
	50					55					60					
TAC	AAC	ACT	CTG	AAC	CCT	GAA	GCA	TCT	GCC	TCG	CCT	TGC	TGC	GTG	ccc	240
Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro	
65					70					75					80	
CAG	GAC	CTG	GAG	ccc	CTG	ACC	ATC	CTG	TAC	TAT	GTT	GGG	AGG	ACC	CCC	288
	Asp															200
	-			85					90	-		_		95		
											•					
	GTG															336
Lys	Val	GIU	100	Leu	Ser	Asn	Met	105	vaı	rys	Ser	Cys	Lys 110	Cys	Ser	
			100					105					110			
(2)	INF	ORMA'	TION	FOR	SEQ	ID :	NO:	8:								
		(i)	SEOU	ENCE	CHA	RACT	ERTS	TICS								
			~					aci								
		(B) T	YPE:	ami.	no a	cid									
		(D) T	OPOL	OGY:	lin	ear									
	122	٠ ، ، ، ،	TDOD		vnn.											
				LE T		-		SEQ	ID N	0: 8	:					
		,														
Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	Thr	Glu	Lys	Asn	Cys	Cys	
1				5					10					15		
Val	Aro	Gln	Len	Tur	Tle	Asr	Phe	Ara	Tare	Aen	Ten	Glu	ייים.	Tare	Trp	
vul	. mg	0111	20	_		7100	1116	25	_	пор	Leo	GLY	30	_	LLP	
Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys	

40

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Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro 65 70 75 80

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro $85 \ 90 \ 95$

Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser 100 105 110

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "recombinant hybrid DNA coding for hybrid TGF-beta2-3"
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: E. coli LC137/pPIMu.TGF-beta2(44/45)beta3
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..132
 - (D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta2"
 - (ix) FEATURE:

- (A) NAME/KEY: mat_peptide(B) LOCATION:133..336
- (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

(A) NAME/KEY: CDS

85

- (B) LOCATION:1..336
- (D) OTHER INFORMATION:/product= "hybrid TGF-beta2-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCT	TTG	GAT	GCG	GCC	TAT	TGC	TTT	AGA	AAT	GTG	CAG	GAT	AAT	TGC	TGC	48
Ala	Leu	Asp	Ala	Ala	Tyr	Cys	Phe	Arg	Asn	Val	Gln	Asp	Asn	Cvs	Cys	10
1				5					10			~		15	-2 -	
CTA	CGT	CCA	CTT	TAC	ATT	GAT	TTC	AAG	AGG	GAT	CTA	GGG	TGG	AAA	TGG	96
									Arg							
			20					25					30	_	-	
ATA	CAC	GAA	CCC	AAA	GGG	TAC	AAT	GCC	AAC	TTC	TGC	TCA	GGC	CCT	TGC	144
Ile	His	Glu	Pro	Lys	Gly	Tyr	Asn	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys	
		35					40					45				
CCA	TAC	CTC	CGC	AGT	GCA	GAC	ACA	ACC	CAC	AGC	ACG	GTG	CTG	GGA	CTG	192
Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu	
	50					55					60					
									GCC							240
Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro	
65					70					75					80	
									TAC							288
Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Val	Gly	Arg	Thr	Pro	

90

95

AAA	GTG	GAG	CAG	CTC	TCC	AAC	ATG	GTG	GTG	AAG	TCT	TGT	AAA	TGT	AGC
Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Val	Val	Lys	Ser	Cys	Lys	Cys	Ser
			100					105					110		
(2)	INFO	RMAT	NOI	FOR	SEQ	ID I	10: 1	10:							
		(i) C	POTT	ENCE	CUAT	a com	20.70	nTOC.	_						
			-	ENCE ENGTH											
		(E		PE:				acre	1.5						
				POL											
	(ii)	MOI	ECUI	E T	PE:	prot	tein								
	(xi)	SEC	QUENC	CE DE	ESCR	PTI	: AC	SEQ :	ID N	0: 10	Ö:				
Ala	Leu	Asp	Ala	Ala	Tyr	Cys	Phe	Arg	Asn	Val	Gln	Asp	Asn	Cys	Cys
1				5					10					15	
*		D	T	m	T1 -		DI			•	. .	61			_
Leu	Arg	PIO	20	Tyr	TTE	Asp	Pne	ьуs 25	Arg	Asp	Leu	GTĀ	30 30	гуѕ	Trp
			20					25					50		
Ile	His	Glu	Pro	Lys	Gly	Tyr	Asn	Ala	Asn	Phe	Cys	Ser	Glv	Pro	Cvs
		35		-	-	_	40				- 2	45	2		-4-
Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu
	50					55					60				
	Asn	Thr	Leu	Asn		Glu	Ala	Ser	Ala		Pro	Cys	Cys	Val	
65					70					75					80
61			03.	_		m).			_	_					_
GIII	Asp	Leu	GIU	Pro 85	Leu	The	TTE	Leu	90	Tyr	vaı	сту	Arg		Pro
				03					90					95	•
Lys	Val	Glu	Gln	Leu	Ser	Asn	Met.	Val	Val	Lvs	Ser	Cvs	Lvs	Cvs	Ser
			100					105				-1-	110	-1-	

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "recombinant hybrid DNA coding for hybrid TGF-beta3-2"

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPIMu.TGF-beta3(44/45)beta2

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..132
- (D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta3"

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 133..336
- (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta2"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..336
- (D) OTHER INFORMATION:/product= "hybrid TGF-beta3-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	Leu	Asp	Thr		Tyr	Cys	Phe	Arg		Leu	Glu	Glu	Asn	Cys	Cys	
1				5					10					15		
GTG	CGC	CCC	CTC	TAC	ATT	GAC	TTC	CGA	CAG	GAT	CTG	GGC	TGG	AAG	TGG	96
Val	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp	Lys	Trp	
			20					25					30			
GTC	CAT	GAA	CCT	AAG	GGC	TAC	TAT	GCC	AAC	ጥጥር	ጥርጥ	CCT	CCA	GCA	mcc.	144
														Ala		144
		35			QL,		40	nia	ASII	rne	Cys		GTĀ	Ата	cys	
		55					40					45				
CCG	TAT	TTA	TGG	AGT	TCA	GAC	ACT	CAG	CAC	AGC	AGG	GTC	CTG	AGC	TTA	192
Pro	$\mathbf{T}\mathbf{y}\mathbf{r}$	Leu	Trp	Ser	Ser	Asp	Thr	Gln	His	Ser	Arg	Val	Leu	Ser	Leu	
	50					55					60					
TAT	AAT	ACC	ATA	AAT	CCA	GAA	GCA	TCT	GCT	TCT	CCT	TGC	TGC	GTG	TCC	240
Tyr	Asn	Thr	Ile	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Ser	
65					70					75					80	
CAA	GAT	TTA	GAA	CCT	CTA	ACC	ATT	CTC	TAC	TAC	ATT	GGC	AAA	ACA	CCC	288
Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Ile	Gly	Lys	Thr	Pro	
				85					90			_	-	95		
AAG	ATT	GAA	CAG	CTT	TCT	AAT	ATG	ATT	GTA	AAG	TCT	TGC	AAA	TGC	AGC	336
Lys	Ile	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Lys	Ser	Cys	Lys	Cys	Ser	
			100					105					110			

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala 1	Leu	Asp	Thr	Asn 5	Tyr	Cys	Phe	Arg	Asn 10	Leu	Glu	Glu	Asn	Cys 15	Cys
Val	Arg	Pro	Leu 20	Tyr	Ile	Asp	Phe	Arg 25	Gln	Asp	Leu	Gly	Trp 30	Lys	Trp
Val	His	Glu 35	Pro	Lys	Gly	Тут	Tyr 40	Ala	Asn	Phe	Cys	Ala 45	Gly	Ala	Cys
Pro	Tyr 50	Leu	Trp	Ser	Ser	Asp 55	Thr	Gln	His	Ser	Arg 60	Val	Leu	Ser	Leu
Tyr 65	Asn	Thr	Ile	Asn	Pro 70	Glu	Ala	Ser	Ala	Ser 75	Pro	Cys	Cys	Val	Ser 80
Gln	Asp	Leu	Glu	Pro 85	Leu	Thr	Ile	Leu	Tyr 90	Tyr	Ile	Gly	Lys	Thr 95	Pro
Lys	Ile	Glu	Gln 100	Leu	Ser	Asn	Met	Ile 105	Val	Lys	Ser	Cys	Lys 110	Cys	Ser